The Value of Chemokine and Chemokine Receptors in Diagnosis, Prognosis, and Immunotherapy of Hepatocellular Carcinoma

1 Supplementary Figures and Tables

1.1 Supplementary Figures

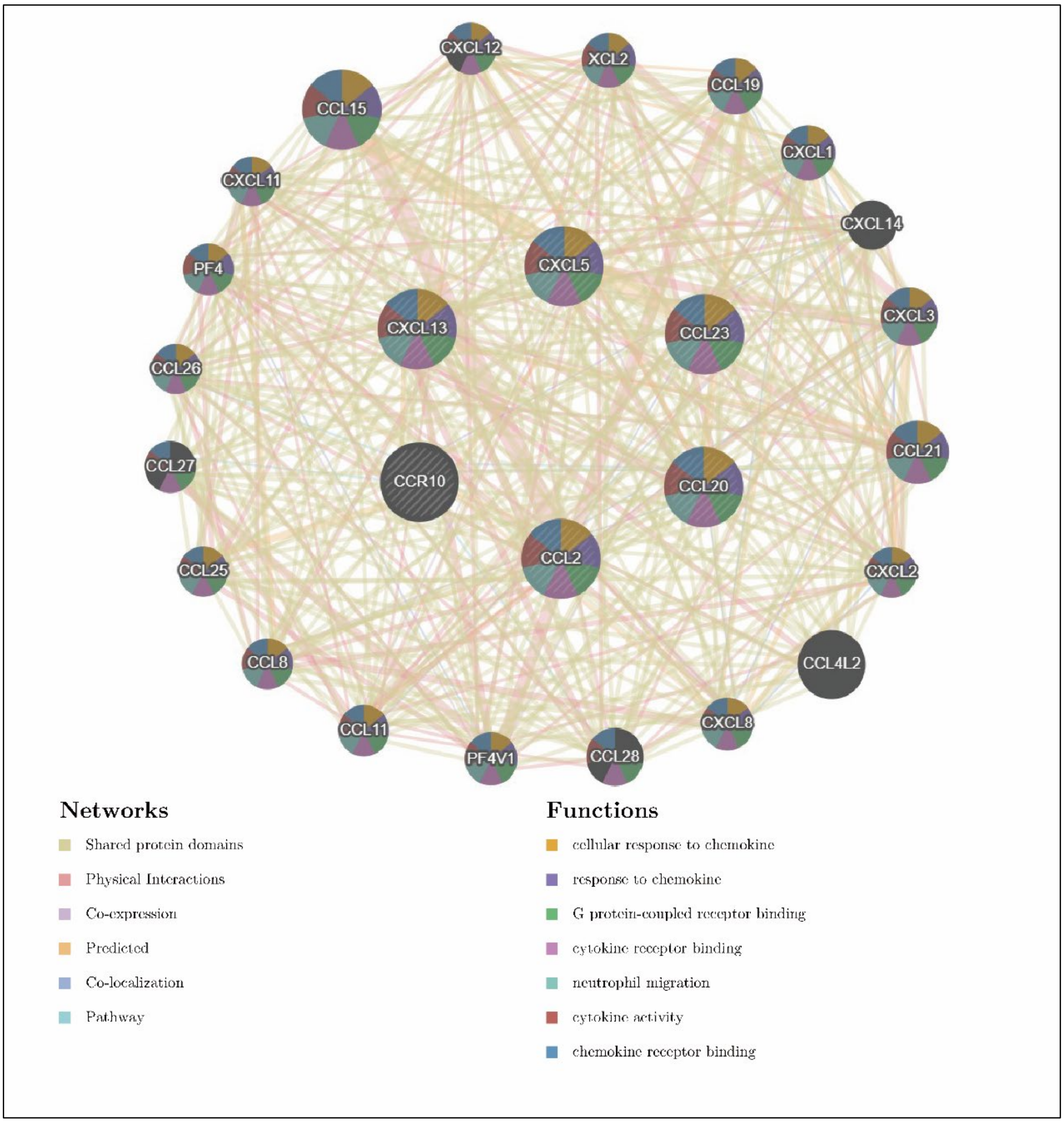


Figure S1 CCRs-related signature genes interaction networks.

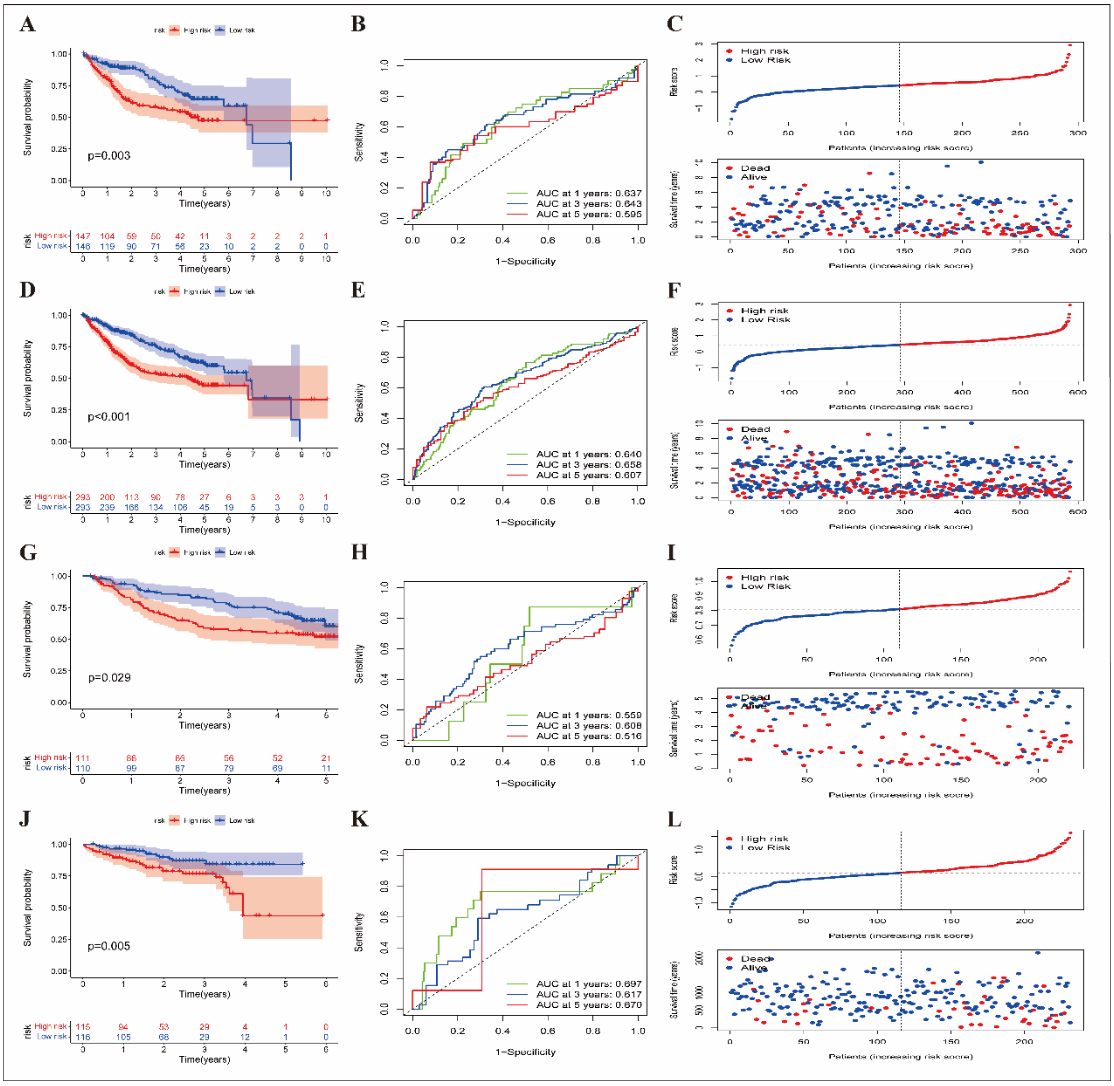


Figure S2 Internal and external validation of CCRs-related gene signature. Kaplan-Meier curves: (**A**)the test set(set2); **(D)** Merged set(set3); **(G)**GSE14520 set(set4); **(J)**ICGC set(set5). ROC curve: **(B)**the test set(set2); **(E)** Merged set(set3); **(H)**GSE14520 set(set4); **(K)**ICGC set(set5). Risk score and survival status distribution: **(C)**in the test set(set2); **(F)** Merged set(set3); **(I)** GSE14520 set(set4); **(L)** ICGC set(set5).

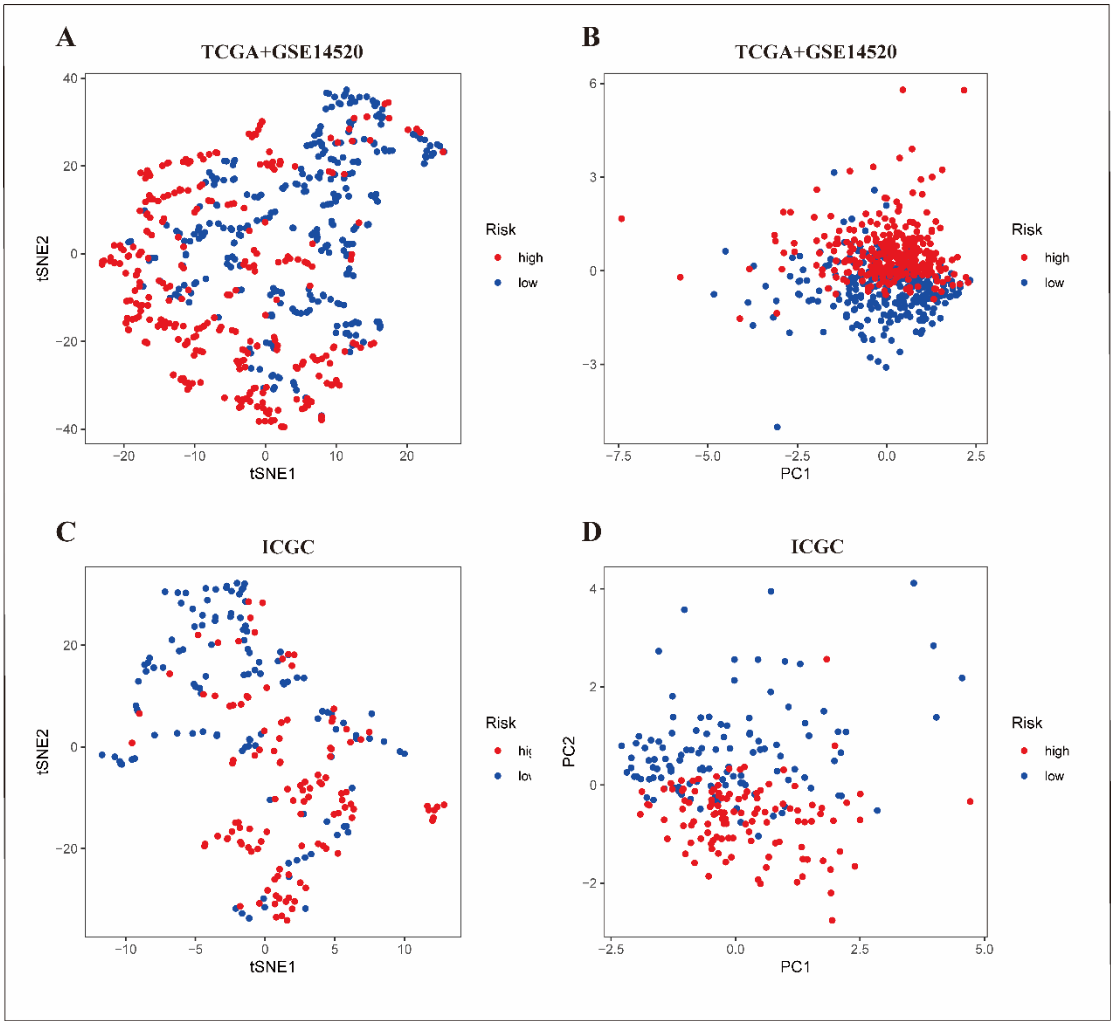


Figure S3 t-SNE and PCA downscaling. (A, B) t-SNE and PCA in the merged set(set3). **(C, D)** t-SNE and PCA in the ICGC set(set5).

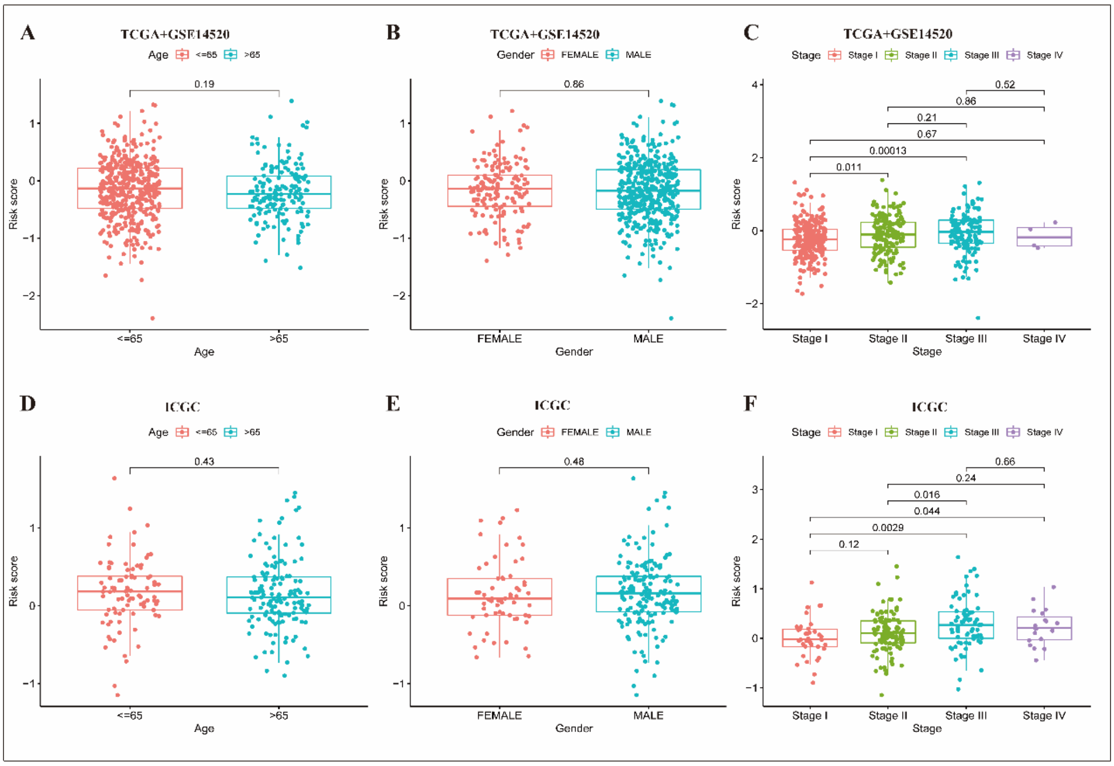


Figure S4 Differences in risk scores between different clinical features.

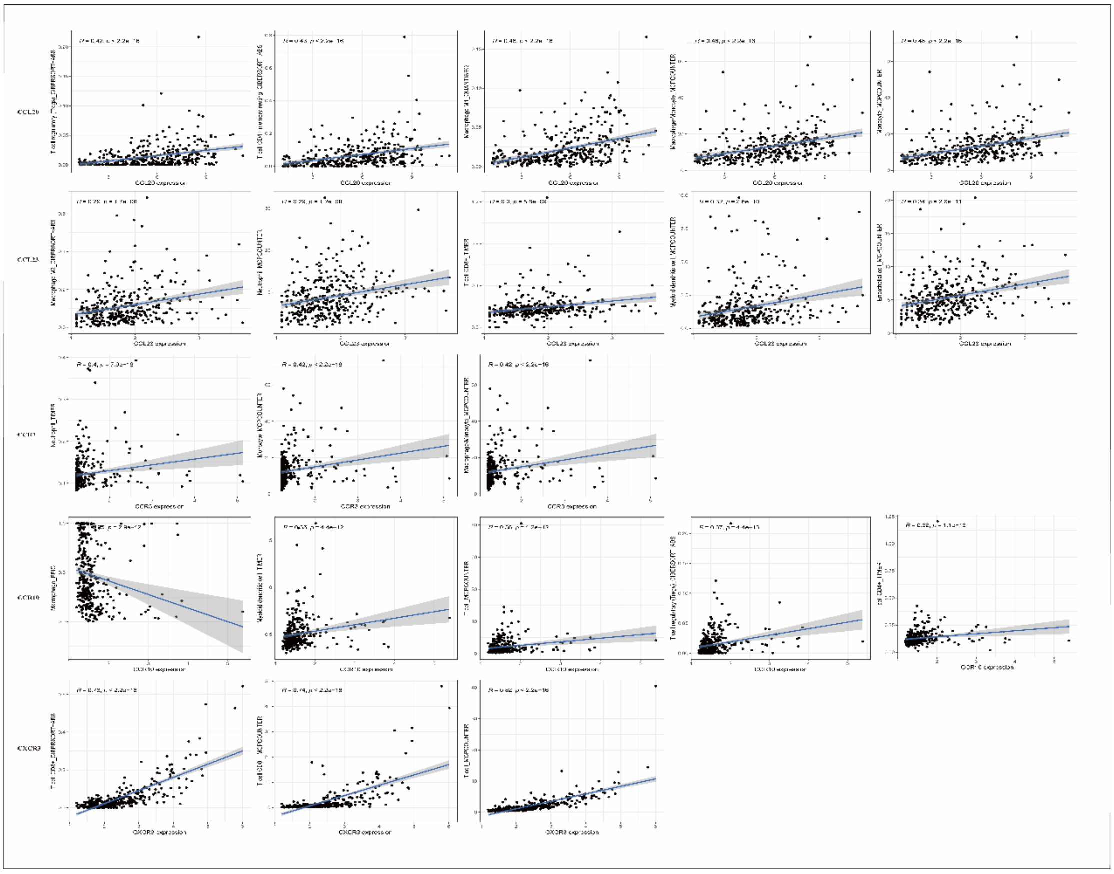


Figure S5 Immune cells in association with CCRs-related signature genes expression.

1 Supplementary Tables

Table S1 Chemokine and Chemokine Receptors related gene

CC	**CXC**	**XC**	**CX3C**	**CCR**	**CXCR**	**XCR**	**CX3CR**
CCL1	CXCL1	XCL1	CX3CL1	CCR1	CXCR1	XCR1	CX3CR1
CCL2	CXCL2	XCL2		CCR2	CXCR2		
CCL3	CXCL3			CCR3	CXCR3		
CCL3L1	PF4			CCR4	CXCR4		
CCL4	PF4V1			CCR5	CXCR5		
CCL4L1	CXCL5			CCR6	CXCR6		
CCL5	CXCL6			CCR7			
CCL7	PPBP			CCR8			
CCL8	CXCL8			CCR9			
CCL11	CXCL9			CCR10			
CCL13	CXCL10			ACKR4			
CCL14	CXCL11						
CCL15	CXCL12						
CCL16	CXCL13						
CCL17	CXCL14						
CCL18	CXCL16						
CCL19	CXCL17						
CCL20							
CCL21							
CCL22							
CCL23							
CCL24							
CCL25							
CCL26							
CCL27							
CCL28							

Table S2 Difference analysis between normal and tumor groups of LIHC

Gene	conMean	treatMean	logFC	pValue	FDR
CCL8	1.811408	3.960043048	1.128404579	9.59E-05	0.000161831
CCL13	0.266178	1.719228075	2.691297707	6.30E-07	1.44E-06
CCL15	2.723552	8.65130615	1.667428551	2.39E-12	1.28E-11
CCL20	17.66611	75.65670856	2.098483614	3.53E-08	1.08E-07
CCL23	5.26949	1.12050107	-2.233519314	9.83E-23	1.41E-21
CCL25	0.421096	69.64127406	7.369649615	3.77E-11	1.80E-10
CCL26	0.116978	1.829557754	3.967185825	6.87E-10	2.27E-09
CCL28	1.136524	4.642807487	2.030369311	0.000216234	0.000344373
PPBP	0.932604	0.355307487	-1.39219653	8.77E-18	9.42E-17
CXCL9	18.377714	39.53501337	1.105173591	0.018280911	0.023820581
CXCL12	80.955124	21.41802086	-1.918297225	3.00E-23	6.44E-22
CXCL14	39.738406	6.842997326	-2.537833715	2.82E-26	1.21E-24
CXCL17	0.182366	5.589944385	4.937925243	1.89E-07	5.42E-07
CCR3	0.019066	0.472138235	4.630135215	7.68E-06	1.50E-05
CCR6	0.014262	0.030172727	1.081068797	0.007454411	0.010339989
CCR8	0.068456	0.292470321	2.09504133	6.36E-07	1.44E-06
CCR10	0.101882	0.489760428	2.265177024	1.50E-12	9.20E-12
CXCR1	1.016872	0.402110695	-1.338473476	1.14E-13	8.20E-13
CXCR2	0.75702	0.308872727	-1.293318926	6.90E-14	5.94E-13
CXCR3	1.25699	3.129562834	1.31598797	6.04E-06	1.30E-05

Table S3 Univariate cox regression for CCRs-related genes

Gene	HR	HR.95L	HR.95H	pValue
CCL20	1.1172623	1.050608305	1.18814511	0.000410834
CCL23	0.6665701	0.48294389	0.92001526	0.01362472
CCL25	0.8826192	0.803773778	0.96919895	0.008916455
CXCL9	0.927391	0.861990224	0.9977538	0.04335942
CCR3	1.2151969	1.016547468	1.45266547	0.03234043
CCR6	1.3400956	1.038686487	1.72896842	0.024325225
CCR10	1.3076637	1.021596588	1.67383517	0.033204995
CXCR3	1.1327998	1.058929358	1.21182342	0.000289884

Table S4 The primer sequences of signature genes

Gene	Forward primer	Reverse primer
CCL20	GCAAGCAACTTTGACTGCTG	TTGGATTTGCGCACACAGAC
CCL23	AGATGACCTTCTCTCATGCTGC	CTCTCCAGGAGTGAACACGG
CCR3	ATGCTGGTGACAGAGGTGAT	AGGTGAGTGTGGAAGGCTTA
CCR10	GGATACTGCCGATCTACTGGC	CCAGGAAGGCGTAGAGAACG
CXCR3	ATGCGAGAGAAGCAGCCTTT	TCCTATAACTGTCCCCGCCA

Original Images for Blots and Gels:

Figure 7A

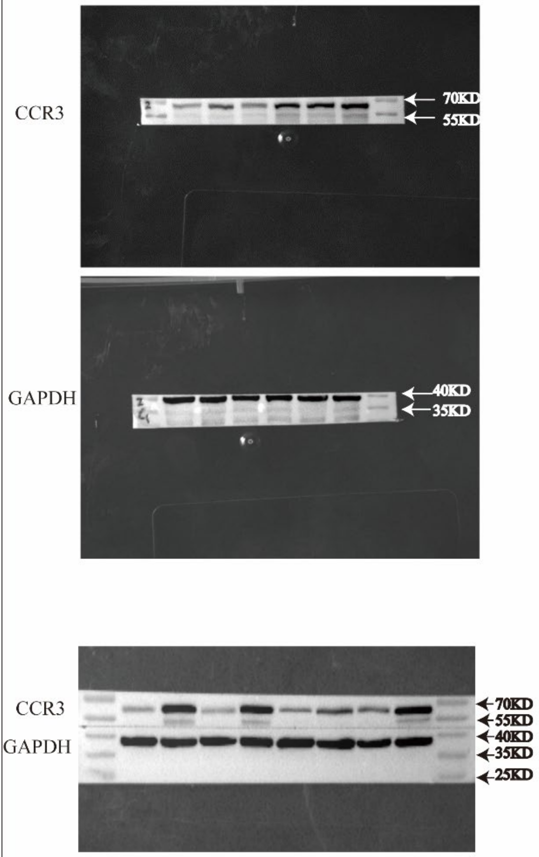
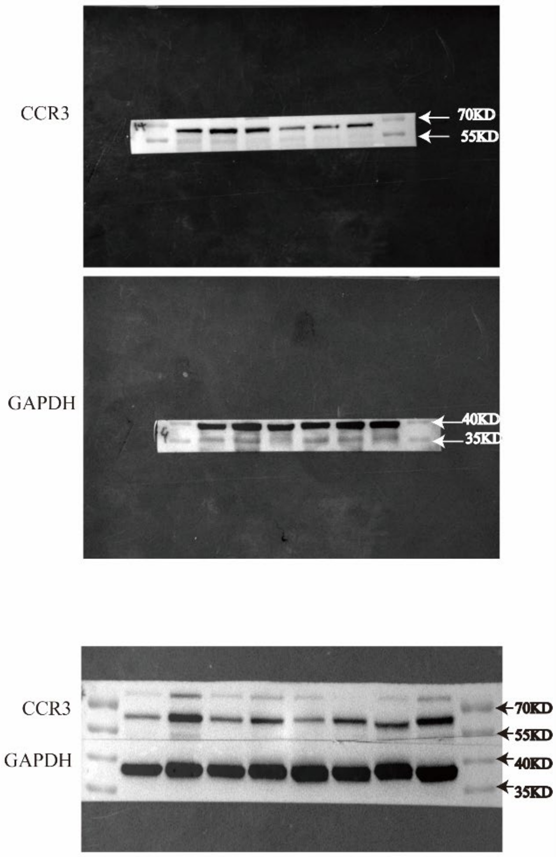


Figure 7C



Ladder: Thermo Scientific PageRuler Prestained Protein Ladder. Catalog Number: 26617